

SACGHS

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# QTL'S

QUANTITATIVE TRAITS

ASSOCIATING DISEASE PHENOTYPES WITH GENOTYPES

VERY DIFFICULT EVEN IN MODEL ORGANISMS

## YEAST ----A MODEL FOR QTL'S

- COMPLETE GENOME SEQUENCE
- ALL POLYMORPHISMS ON A CHIP
- NO ETHICAL CONCERNS ABOUT BACKCROSSES

Steinmetz L. et al. (2002) Dissecting the architecture of a quantitative trait locus in yeast. *NATURE* **416**:326.

# FIGURE 1. Analysis of the high-temperature-growth phenotype (Htg).

QuickTime™ and a  
TIFF (Uncompressed) decompressor  
are needed to see this picture.

## HEAT RESISTANCE MAPPED TO 32 kb OF CHROM. IV (3444 MARKERS)

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TIFF (Uncompressed) decompressor  
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**FIGURE 3. QTL between YJM789 (YJM145 genetic background), S96 (S288c background) and five other Htg+ and six other Htg- yeast strains.**

QuickTime™ and a  
TIFF (Uncompressed) decompressor  
are needed to see this picture.

## CONCLUSIONS OF THE BEST YEAST STUDY

*“The fact that neither single allele is necessary or sufficient for high temperature growth explains the lack of marker-trait association”*

*“Combinations of both common and rare variants are likely to underlie quantitative traits and the number of genes could be far greater than expected.”*

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